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RAW SEQUENCE LISTING

DATE: 03/27/2002

PATENT APPLICATION: US/09/836,911A

TIME: 14:35:31

Input Set : A:\402iseq.002

Output Set: N:\CRF3\03272002\I836911A.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Hadlaczky, Gyula
7 Szalay, Aladar
9 (ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
10 AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
12 (iii) NUMBER OF SEQUENCES: 34
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Heller Ehrman White & McAuliffe
16 (B) STREET: 4350 La Jolla Village Drive, 6th Floor
17 (C) CITY: San Diego
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 92122
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Diskette
24 (B) COMPUTER: IBM Compatible
25 (C) OPERATING SYSTEM: DOS
26 (D) SOFTWARE: FastSEQ Version 1.5
28 (vi) CURRENT APPLICATION DATA:
C--> 29 (A) APPLICATION NUMBER: US/09/836,911A
C--> 30 (B) FILING DATE: 17-Apr-2002
31 (C) CLASSIFICATION:
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 08/835,682
35 (B) FILING DATE: 10-APR-1997
36 (A) APPLICATION NUMBER: 08/695,191
37 (B) FILING DATE: 07-AUG-1996
38 (A) APPLICATION NUMBER: 08/682,080
39 (B) FILING DATE: 15-JUL-1996
40 (A) APPLICATION NUMBER: 08/629,822
41 (B) FILING DATE: 10-APR-1996
43 (viii) ATTORNEY/AGENT INFORMATION:
44 (A) NAME: Seidman, Stephanie L
45 (B) REGISTRATION NUMBER: 33,779
46 (C) REFERENCE/DOCKET NUMBER: 24601-402I
49 (ix) TELECOMMUNICATION INFORMATION:
50 (A) TELEPHONE: 858-450-8403
51 (B) TELEFAX: 858-587-5360
52 (C) TELEX:
54 (2) INFORMATION FOR SEQ ID NO: 1:
56 (i) SEQUENCE CHARACTERISTICS:
57 (A) LENGTH: 1293 base pairs

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58      (B) TYPE: nucleic acid
59      (C) STRANDEDNESS: single
60      (D) TOPOLOGY: linear
62      (ii) MOLECULE TYPE: Genomic DNA
63      (iii) HYPOTHETICAL: NO
64      (iv) ANTI-SENSE: NO
W--> 65      (v) FRAGMENT TYPE:
66      (vi) ORIGINAL SOURCE:
67      (ix) FEATURE:
69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71  GAATTCATCA TTTTTCANGT CCTCAAGTGG ATGTTTCTCA TTTNCCATGA TTTTAAGTTT      60
72  TCTCGCCATA TTCCTGGTCC TACAGTGTGC ATTTCTCCAT TTTNCACGTT TTNCAGTGAT      120
73  TTCGTCATTT TCAAGTCCTC AAGTGGATGT TTCTCATTTN CCATGAATTT CAGTTTTCTN      180
74  GCCATATTCC ACGTCCTACA GNGGACATTT CTAAATTTNC CACCTTTTTT AGTTTTCTCTC      240
75  GCCATATTTC ACGTCCTAAA ATGTGTATTT CTCGTTTNNC GTGATTTTCA GTTTTCTCGC      300
76  CAGATTCAGG GTCCTATAAT GTGCATTTCT CATTNNNCAC GTTTTTCAGT GATTTTCGTCA      360
77  TTTTTCGAAG TCGGCAAGTG GATGTTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAAT      420
78  ATTCCATGTC CTACAATGAT CATTTTTAAT TTTCCACCTT TTCATTTTTC CACGCCATAT      480
79  TTCATGTCCT AAAGTGATA TTTCTCCTTT TCCGCGATTT TCAGTTTTCT CGCCATATTC      540
80  CAGGTCCTAC AGTGTGCATT CCTCATTTTT CACCTTTTTT ACTGATTTTCG TCATTTTTTCA      600
81  AGTCGTC AAC TGGATCTTTC TAATTTTCCA TGATTTTTCAG TTATCTTGTC ATATTCCATG      660
82  TCCTACAGTG GACATTTCTA AATTTTCCAA CTTTTTCAAT TTTTCTCGAC ATATTGACG      720
83  TGCTAAAGTG TGTATTTCTT ATTTTCCGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGTC      780
84  CTAATAGTGT GCATTTCTCA TTTTTCACGT TTTTCAGTGA TTTTCGTCATT TTTTCCAGTT      840
85  GTCAAGGGGA TGTTTCTCAT TTTCCATGAG TGTCAGTTTT CTTGCTATAT TCCATGTCCT      900
86  ACAGTGACAT TTCTAAATAT TATACCTTTT TCAGTTTTTC TCACCATATT TCACGTCCTA      960
87  AAGTATATAT TTCTCATTTT CCCTGATTTT CAGTTTCTCT GCCATATTCC AGGTCCTACA      1020
88  GTGTGCATTT CTCATTTTTT ACGTTTTTCA GTAATTTCTT CATTTTTTTAA GCCCTCAAAT      1080
89  GGATGTTTCT CATTTTCCAT GATTTTTCAGT TTTCTTGCCA TATACCATGT CCTACAGTGG      1140
90  ACATTTCTAA ATTATCCACC TTTTTCAGTT TTTTCATCGGC ACATTTTCACG TCCTAAAGTG      1200
91  TGTATTTCTA ATTTTTCAGT ATTTTTCAGT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG      1260
92  CATTCTCAT TTTTTCAGTT TTTTCAGTGA TTC      1293
94  (2) INFORMATION FOR SEQ ID NO: 2:
96      (i) SEQUENCE CHARACTERISTICS:
97          (A) LENGTH: 1044 base pairs
98          (B) TYPE: nucleic acid
99          (C) STRANDEDNESS: single
100         (D) TOPOLOGY: linear
102         (ii) MOLECULE TYPE: Genomic DNA
103         (iii) HYPOTHETICAL: NO
104         (iv) ANTI-SENSE: NO
W--> 105         (v) FRAGMENT TYPE:
106         (vi) ORIGINAL SOURCE:
107         (ix) FEATURE:
109         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
111  AGGCTATGG TGAAAAGGA AATATCTTCC CCTGAAACT AGACAGAAGG ATTCTCAGAA      60
112  TCTTATTTGT GATGTGCGCC CCTCAACTAA CAGTGTTGAA GCTTCTTTT GATAGAGCAG      120
113  TTTTGAAACA CTCTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTT      180
114  CGTTGGAAAC GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT      240

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115 TGGGATGTTT CAGTTGAAGT CACAGTGTG AACAGTCCCC TTTTCATAGAG CAGGTTTGAA 300
116 ACACTCTTTT TTGTAGTATC TGGAAAGTGA CATTGAGGAG GATCTCAGGA CTGCGGTGAA 360
117 AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT 420
118 GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTTG AAACACTCTT 480
119 TTTGTGGAAT CTGCAAGTGG ATATTTGTCT AGCTTTGAGG ATTTGTTGG GAAACGGGAT 540
120 TACATATAAA AAGCAGACAG CAGCATTCCC AGAAACTTCT TTGTGATGTT TGCATTCAAG 600
121 TCACAGAGTT GAACATTCCC TTTTCATAGAG CAGGTTTGAA ACACACTTTT TGATGTATCT 660
122 GGATGTGGAC ATTTGCAGCG CTTTCAGGCC TAAGGTGAAA AGGAAATATC TTCCCCTGAA 720
123 AACTAGACAG AAGCATTCTC AGAAACTTAT TTGTGATGTG CGCCCTCAAC TAACAGTGTT 780
124 GAAGCTTTCT TTTGATAGAG GCAGTTTGA AACACTCTTT TGTGGAATCT GCAAGTGGAT 840
125 ATTTGTCTAG CTTTGAGGAT TTCTTTGGAA ACGGGATTAC ATATAAAAAG CAGACAGCAG 900
126 CATTCCCAGA ATCTTGTTTG TGATGTTTGC ATTCAAGTCA CAGAGTTGAA CATTCCCTTT 960
127 CAGAGAGCAG GTTTGAACAC TCTTTTTATA GTATCTGGAT GTGGACATTT GGAGCGCTTT 1020
128 CAGGGGGGAT CCTCTAGAAT TCCT 1044

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2492 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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W--> 149 CTGCAGCTGG GGGTCTCCAA TCAGGCAGGG GCCCCTTACT ACTCAGATGG GGTGGCCGAG 60
150 TAGGGGAAGG GGGTGCAGGC TGCATGAGTG GACACAGCTG TAGGACTACC TGGGGGCTGT 120
151 GGATCTATGG GGGTGGGGAG AAGCCCAGTG ACAGTGCCTA GAAGAGACAA GGTGGCCTGA 180
152 GAGGGTCTGA GGAACATAGA GCTGGCCATG TTGGGGCCAG GTCTCAAGCA GGAAGTGAGG 240
153 AATGGGACAG GCTTGAGGAT ACTCTACTCA GTAGCCAGGA TAGCAAGGAG GGCTTGGGGT 300
154 TGCTATCCTG GGGTTCAACC CCCCAGGTTG AAGGCCCTGG GGGAGATGGT CCCAGGACAT 360
155 ATTACAATGG ACACAGGAGG TTGGGACACC TGGAGTCACC AAACAAAACC ATGCCAAGAG 420
156 AGACCATGAG TAGGGGTGTC CAGTCCAGCC CTCTGACTGA GCTGCATTGT TCAAATCCAA 480
157 AGGGCCCCCTG CTGCCACCTA GTGGCTGATG GCATCCACAT GACCCTGGGC CACACGCGTT 540
158 TAGGGTCTCT GTGAAGACCA AGATCCTTGT TACATTGAAC GACTCCTAAA TGAGCAGAGA 600
159 TTTCCACCTA TTCGAAACAA TCACATAAAA TCCATCCTGG AAAAAGCCTG GGGGATGGCA 660
160 CTAAGGCTAG GGATAGGGTG GGATGAAGAT TATAGTTACA GTAAGGGGTT TAGGGTTAGG 720
161 GATCAACGTT GGTTAGGAGT TAGGGATACA GTAGGGTACC GGTAGGGTTA GGGGTTAGGG 780
162 TTAGGGGTTA GGGTTAGGGT TAGGGTTAGG GTTAGGGTTA GGGGTTAGGG GTTAGGGTTA 840
163 GGGTTAGGTT TTGGGGTGGC GTATTTTGGT CTTATACGCT GTGTTCCACT GGCAATGAAA 900
164 AGAGTTCTTG TTTTTCCTTC AGCAATTTGT CATTTTAAA AGAGTTTAGC AATTCTAACA 960
165 GATATAGACC AGCTGTGCTA TCTCATTGTG GTTTTCAATT GTAACCACAT TGTGGTTTCA 1020
166 ATGTGTTTAC TTGCCATCTG TAGATCTTCT TTGCGTGAGG TGTCTGTTCA GATGTGTGTG 1080
167 CATTTCTTGN NTTTTNGGCTG TTTAACTTAT TGTTTAGTTT TAATAATTTT TTATATATTT 1140
168 GAAGACAAAT CTTTCTCAGA TGTGTATTTG CAAATATTTT TTCAATATGA GGCTTGCTTT 1200
169 TGTCTCTAAC AAGGTCTCTT CAGAGATAAC TTAAATATAA GAAATCCACA CTGTCACTTC 1260
170 TTTTGTGTAT ATCTACCTTT TGTGTCATTT GTTAAAATTC ATTACCAAAC CCAAAGGCAG 1320

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171 ATAGCTTTTC TTCTATTGTT TCTTCTAGAA ATTTGTATAG TTTTGCATTT TTAGTGTAAG 1380
172 GATGATTTTG AGTGATTATT TGTGTAAGTT GTAAAGTTTT CGTCTATATC CATATCATTT 1440
173 CTTATGGTTT CCAATTAATC GTTCCCTCAC TATTTTGGG AAAGACACAG GATAGTGGGC 1500
174 TTTGTTAGAG TAGATAGGTA GCTAGACATG AACAGGAGGG GGCCTCCTGG AAAAGGGAAA 1560
175 GTCTGGGAAG GCTCACCTGG AGGACCACCA AAAATTCACA TATTAGTAGC ATCTCTAGTG 1620
176 CTGGAGTGGA TGGGCACTTG TCAATTGTGG GTAGGAGGGA AAAGAGGTCC TATGCAGAAA 1680
177 GAAACTCCCT AGAACTCCTC TGAAGATGCC CCAATCATTC ACTCTGCAAT AAAAATGTCA 1740
178 GAATATTGCT AGCTACATGC TGATAAGGNN AAAGGGGACA TTCTTAAGTG AAACCTGGCA 1800
179 CCATAAGTAC AGATTAGGGC AGAGAAGGAC ATTCAAAAGA GGCAGGCGCA GTAGGTACAA 1860
180 ACGTGATCGC TGTCAGTGTG CCTGGGATGG CGGGAAGGAG GCTGGTGCCA GAGTGGATTC 1920
181 GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCCCACAA GCCTAAGTGG 1980
182 GGCAAGTTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT 2040
183 TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGA CTCTTAG 2100
184 GCTGTTTAAT GCATCGCTCA GTCCCACTCC TCCCTATTTT TCTACAATAA ACTCTTTACA 2160
185 CTGTGTTTCT TTTCAATGAA GTTATCTGCC ATCTTTGTAT TGCCTCTTGG TGAAAATGTT 2220
186 TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT 2280
187 TTGAATTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG 2340
188 CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCAT CTGCCCAGAG GTGGCGGCTG 2400
189 CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCAAG CTGCCAGCAG GGGGCGTACG 2460
190 ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG 2492

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192 (2) INFORMATION FOR SEQ ID NO: 4:

194 (i) SEQUENCE CHARACTERISTICS:

195 (A) LENGTH: 28 base pairs

196 (B) TYPE: nucleic acid

197 (C) STRANDEDNESS: single

198 (D) TOPOLOGY: linear

200 (ii) MOLECULE TYPE: Genomic DNA

201 (iii) HYPOTHETICAL: NO

202 (iv) ANTI-SENSE: NO

W--> 203 (v) FRAGMENT TYPE:

204 (vi) ORIGINAL SOURCE:

205 (ix) FEATURE:

207 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

209 GGGGAATTCA TTGGGATGTT TCAGTTGA 28

211 (2) INFORMATION FOR SEQ ID NO: 5:

213 (i) SEQUENCE CHARACTERISTICS:

214 (A) LENGTH: 29 base pairs

215 (B) TYPE: nucleic acid

216 (C) STRANDEDNESS: single

217 (D) TOPOLOGY: linear

W--> 219 (ii) MOLECULE TYPE: DNA

220 (iii) HYPOTHETICAL: NO

221 (iv) ANTI-SENSE: NO

W--> 222 (v) FRAGMENT TYPE:

223 (vi) ORIGINAL SOURCE:

224 (ix) FEATURE:

226 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

228 CGAAAGTCCC CCCTAGGAGA TCTTAAGGA 29

230 (2) INFORMATION FOR SEQ ID NO: 6:

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Input Set : A:\402iseq.002

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232      (i) SEQUENCE CHARACTERISTICS:
233          (A) LENGTH: 47 base pairs
234          (B) TYPE: nucleic acid
235          (C) STRANDEDNESS: single
236          (D) TOPOLOGY: linear
W--> 238      (ii) MOLECULE TYPE: Gemonic DNA
239      (iii) HYPOTHETICAL: NO
240      (iv) ANTI-SENSE: NO
W--> 241      (v) FRAGMENT TYPE:
242      (vi) ORIGINAL SOURCE:
243      (ix) FEATURE:
245      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
247 CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC      47
251 (2) INFORMATION FOR SEQ ID NO: 7:
253      (i) SEQUENCE CHARACTERISTICS:
254          (A) LENGTH: 25 base pairs
255          (B) TYPE: nucleic acid
256          (C) STRANDEDNESS: single
257          (D) TOPOLOGY: linear
259      (ii) MOLECULE TYPE: Genomic DNA
260      (iii) HYPOTHETICAL: NO
261      (iv) ANTI-SENSE: NO
W--> 262      (v) FRAGMENT TYPE:
263      (vi) ORIGINAL SOURCE:
264      (ix) FEATURE:
266      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
268 CGATTAAAT TAATTAAGCC CGGGC      25
271 (2) INFORMATION FOR SEQ ID NO: 8:
273      (i) SEQUENCE CHARACTERISTICS:
274          (A) LENGTH: 27 base pairs
275          (B) TYPE: nucleic acid
276          (C) STRANDEDNESS: single
277          (D) TOPOLOGY: linear
279      (ii) MOLECULE TYPE: Genomic DNA
280      (iii) HYPOTHETICAL: NO
281      (iv) ANTI-SENSE: NO
W--> 282      (v) FRAGMENT TYPE:
283      (vi) ORIGINAL SOURCE:
284      (ix) FEATURE:
286      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
288 TAAATTTAAT TAATTCGGGC CCGTCGA      27
290 (2) INFORMATION FOR SEQ ID NO: 9:
292      (i) SEQUENCE CHARACTERISTICS:
293          (A) LENGTH: 69 base pairs
294          (B) TYPE: nucleic acid
295          (C) STRANDEDNESS: single
296          (D) TOPOLOGY: linear
298      (ii) MOLECULE TYPE: Genomic DNA
301      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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PATENT APPLICATION: US/09/836,911A

TIME: 14:35:32

Input Set : A:\402\seq.002

Output Set: N:\CRF3\03272002\I836911A.raw

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L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:69 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1
L:65 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1
L:109 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2
L:105 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2
L:147 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=3
L:143 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3
L:207 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=4
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L:245 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=6
L:238 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:241 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6
L:266 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=7
L:262 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7
L:286 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=8
L:282 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8
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L:299 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq 9, (D) OTHER INFORMATION:
L:331 M:220 C: Keyword misspelled or invalid format, [(H) DOCUMENT NUMBER:]
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L:2034 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33

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